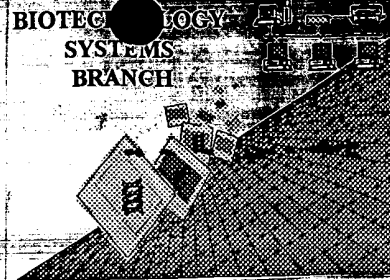


**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer-readable form:

Application Serial Number: 09/380,419  
Source: 1655  
Date Processed by STIC: 12/20/2000

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/380,419

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8        Skipped Sequences (OLD RULES)      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences (NEW RULES)      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10        Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism (NEW RULES)      Sequence(s)        are missing this mandatory field or its response.
- 12        Use of <220>Feature (NEW RULES)      Sequence(s)        are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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J. Goldberg

1655

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/380,419

DATE: 12/20/2000  
TIME: 15:02:54

Input Set : A:\MC4R.txt  
Output Set: N:\CRF3\12202000\I380419.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Rothschild, Max F.  
4 Kim, Kwan Suk  
5 Emmett, Rebecca S.  
7 <120> TITLE OF INVENTION: Melanocortin-4 Receptor Gene and Use as a Genetic  
8 Marker for Fat Content, Weight Gain, and/or Feed  
9 Consumption in Animals  
11 <130> FILE REFERENCE: rothshcild mc4r2  
13 <140> CURRENT APPLICATION NUMBER: 09/380,419  
14 <141> CURRENT FILING DATE: 2000-07-24  
16 <150> PRIOR APPLICATION NUMBER: PCT/US99/16862  
17 <151> PRIOR FILING DATE: 1999-07-26  
19 <160> NUMBER OF SEQ ID NOS: 26  
21 <170> SOFTWARE: PatentIn Ver. 2.0

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ERRORED SEQUENCES

23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 745  
25 <212> TYPE: DNA  
26 <213> ORGANISM: porcine  
28 <220> FEATURE:  
29 <221> NAME/KEY: variation  
30 <222> LOCATION: (678)  
31 <223> OTHER INFORMATION: G/A  
33 <400> SEQUENCE: 1  
34 acaagaatct gcattcaccr atgtactttt tcatctgtag cctggtctgt gctgatatgc 60  
35 tggtagcggt ttccaatggg tcagaaacca ttgtcatcac cctattaaac agcaygaca 120  
36 cggacgcaca gagtttcaca gtgaatttlg ataatgcat tgactcagtg atctgtagct 180  
37 ccttaactcg ctaaatgtgc agcctgcttt cgattgcagt ggacaqqtat tttactatct 240  
38 ttatgtctct ccagtaccat aacattatga cagttlaagc ggttggaaac atcatcagtt 300  
39 gtaactgggc agtetgcacg gtgtcgggtg ttttgttcat catttactca gatagcagty 360  
40 ctgttattat ctgctcaca accgtgttct taccatgct ggcctcctat gcttctctct 420  
41 atgtccacat gtctctcatg gccagactcc acattaagag gatcgccgtc ctcccaaggc 480  
42 ctggcaccat ccgccaaggt gccaacatga agggggcaat taccctgacc atcttgatty 540  
43 gggctcttlt ggtctgctgg gcccccttct tccctcactt aatattctat atctcctgcc 600  
44 cccagaatcc atactgtgtg tgcctcatgt ctcactttaa ttgtatctc atcctgatca 660  
45 tgtgtaatc catcatcgtt cccttgattt atgcaactcc gagccaagaa ctgaggaaaa 720  
E--> 46 ccttcaaaga gatcatctgt tgetat 746

746 shown

Per Sequence Rules, use "r" to represent  
g or a; "g" can  
only represent  
itself

see next pages for more errors

09/380,419 2

<210> 3  
<211> 311  
<212> PRT  
<213> Homo sapiens

see p. 3

<400> 3  
Gln Leu Phe Val Ser Pro Glu Val Phe Val Thr Leu Gly Val Ile Ser  
1 5 10 15  
Leu Leu Glu Asn Ile Leu Val Ile Val Ala Ile Ala Lys Asn Lys Asn  
20 25 30  
Leu His Ser Pro Met Tyr Phe Phe Ile Cys Ser Leu Ala Val Ala Asp  
35 40 45  
Met Leu Val Ser Val Ser Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu  
50 55 60  
Leu Asn Ser Thr Asp Thr Asp Ala Gln Ser Phe Thr Val Asn Ile Asp  
65 70 75 80  
Asn Val Ile Asp Ser Val Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys  
85 90 95  
Ser Leu Leu Ser Ile Ala Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala  
100 105 110  
Leu Gln Tyr His Asn Ile Met Thr Val Lys Arg Val Gly Ile Ser Ile  
115 120 125  
Ser Cys Ile Trp Ala Ala Cys Thr Val Ser Gly Ile Leu Phe Ile Ile  
130 135 140  
Tyr Ser Asp Ser Ser Ala Val Ile Ile Cys Leu Ile Thr Met Phe Phe  
145 150 155 160  
Thr Met Leu Ala Leu Met Ala Ser Leu Tyr Val His Met Phe Leu Met  
165 170 175  
Ala Arg Leu His Ile Lys Arg Ile Ala Val Leu Pro Gly Thr Gly Ala  
180 185 190  
Ile Arg Gln Gly Ala Asn Met Lys Gly Ala Ile Thr Leu Thr Ile Leu  
195 200 205  
Ile Gly Val Phe Val Val Cys Trp Ala Pro Phe Phe Leu His Leu Ile  
210 215 220  
Phe Tyr Ile Ser Cys Pro Gln Asn Pro Tyr Cys Val Cys Phe Met Ser  
225 230 235 240  
His Phe Asn Leu Tyr Leu Ile Leu Ile Met Cys Asn Ser Ile Ile Asp  
245 250 255  
Pro Leu Ile Tyr Ala Leu Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys  
260 265 270

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09/380,419 3

Glu Ile Ile Cys Cys Tyr Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser  
275 280 285

Arg Tyr Ala Pro Pro Glu Asn Asp Ile Xaa Val Ile Cys Asn Phe Ile  
290 295 300

Asp Glu Asn Thr Ile Ala Leu  
305 310

See Item 10 on Enol  
Summary Sheet

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/380,419

DATE: 12/20/2000

TIME: 15:02:55

Input Set : A:\MC4R.txt

Output Set: N:\CRF3\12202000\I380419.raw

L:46 M:252 E: No. of Seq. differs. <211>LENGTH:Input:745 Found:746 SEQ:1  
L:129 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:129 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3  
L:129 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3  
L:129 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
L:129 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3